

RAW SEQUENCE LISTING

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Application Serial Number: 10598671

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ENTERED

<110> APPLICANT: The UAB Research Foundation
 MARTIN, Michael
 <120> TITLE OF INVENTION: Methods and Compositions Related to
 Regulation of Cytokine Production by Glycogen Synthase
 Kinase 3 (GSK-3)
 <130> FILE REFERENCE: 21085.0072P1

 <140> CURRENT APPLICATION NUMBER:10598671
 <141> CURRENT FILING DATE:0001-01-01
 <150> PRIOR APPLICATION NUMBER: PCT/US05/07586
 <151> PRIOR FILING DATE: 2005-03-17
 <150> PRIOR APPLICATION NUMBER: 60/551,646
 <151> PRIOR FILING DATE: 2004-03-09
 <160> NUMBER OF SEQ ID NOS: 6
 <170> SOFTWARE: FastSEQ for Windows Version 4.0

 <210> SEQ ID NO 1
 <211> LENGTH: 483
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
 synthetic construct
 <400> SEQUENCE: 1

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Gly	Gly	Gly	Pro	Gly	Gly	Ser	Ala	Ser	Gly	Pro	Gly	Gly	Thr	Gly	Gly	35	40	45	
Gly	Lys	Ala	Ser	Val	Gly	Ala	Met	Gly	Gly	Gly	Val	Gly	Ala	Ser	Ser	50	55	60	
Ser	Gly	Gly	Gly	Pro	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Pro	65	70	75	80
Gly	Ala	Gly	Thr	Ser	Phe	Pro	Pro	Pro	Gly	Val	Lys	Leu	Gly	Arg	Asp	85	90	95	
Ser	Gly	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Glu	100	105	110	
Arg	Ser	Gln	Glu	Val	Ala	Tyr	Thr	Asp	Ile	Lys	Val	Ile	Gly	Asn	Gly	115	120	125	
Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Arg	Leu	Ala	Glu	Thr	Arg	Glu	Leu	130	135	140	
Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg	Glu	145	150	155	160
Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu	Arg	165	170	175	
Tyr	Phe	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Leu	Tyr	Leu	Asn	180	185	190	
Leu	Val	Leu	Glu	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg	His	195	200	205	
Phe	Thr	Lys	Ala	Lys	Leu	Thr	Ile	Pro	Ile	Leu	Tyr	Val	Lys	Val	Tyr	210	215	220	
Met	Tyr	Gln	Leu	Phe	Arg	Ser	Leu	Ala	Tyr	Ile	His	Ser	Gln	Gly	Val	225	230	235	240
Cys	His	Arg	Asp	Ile	Lys	Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Asp	Thr	245	250	255	
Ala	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Arg	260	265	270	
Gly	Glu	Pro	Asn	Val	Ser	Tyr	Ile	Cys	Ser	Arg	Tyr	Tyr	Arg	Ala	Pro	275	280	285	
Glu	Leu	Ile	Phe	Gly	Ala	Thr	Asp	Tyr	Thr	Ser	Ser	Ile	Asp	Val	Trp				

290		295		300											
Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Ile	Phe
305					310					315					320
Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu
				325						330				335	
Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr	Thr
			340					345					350		
Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Val	Phe
		355					360					365			
Lys	Ser	Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Ser	Leu	Leu
	370					375					380				
Glu	Tyr	Thr	Pro	Ser	Ser	Arg	Leu	Ser	Pro	Leu	Glu	Ala	Cys	Ala	His
385					390					395					400
Ser	Phe	Phe	Asp	Glu	Leu	Arg	Cys	Leu	Gly	Thr	Gln	Leu	Pro	Asn	Asn
			405						410					415	
Arg	Pro	Leu	Pro	Pro	Leu	Phe	Asn	Phe	Ser	Ala	Gly	Glu	Leu	Ser	Ile
			420					425					430		
Gln	Pro	Ser	Leu	Asn	Ala	Ile	Leu	Ile	Pro	Pro	His	Leu	Arg	Ser	Pro
		435					440					445			
Ala	Gly	Thr	Thr	Thr	Leu	Thr	Pro	Ser	Ser	Gln	Ala	Leu	Thr	Glu	Thr
	450					455					460				
Pro	Thr	Ser	Ser	Asp	Trp	Gln	Ser	Thr	Asp	Ala	Thr	Pro	Thr	Leu	Thr
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<210> SEQ ID NO 2

<211> LENGTH: 420

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct

<400> SEQUENCE: 2

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			20					25					30		
Asp	Gly	Ser	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Pro	Gly	Gln	Gly	Pro
	35						40					45			
Asp	Arg	Pro	Gln	Glu	Val	Ser	Tyr	Thr	Asp	Thr	Lys	Val	Ile	Gly	Asn
	50					55					60				
Gly	Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Lys	Leu	Cys	Asp	Ser	Gly	Glu
65				70						75				80	
Leu	Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg
			85					90						95	
Glu	Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu
	100						105						110		
Arg	Tyr	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Val	Tyr	Leu	
	115					120					125				
Asn	Leu	Val	Leu	Asp	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg
	130				135						140				
His	Tyr	Ser	Arg	Ala	Lys	Gln	Thr	Leu	Pro	Val	Ile	Tyr	Val	Lys	Leu
145				150						155				160	
Tyr	Met	Tyr	Gln	Leu	Phe	Arg	Ser	Leu	Ala	Tyr	Ile	His	Ser	Phe	Gly
			165					170						175	
Ile	Cys	His	Arg	Asp	Ile	Lys	Pro	Gln	Asn	Leu	Leu	Leu	Asp	Pro	Asp
		180						185					190		
Thr	Ala	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val
	195					200						205			
Arg	Gly	Glu	Pro	Asn	Val	Ser	Tyr	Ile	Cys	Ser	Arg	Tyr	Tyr	Arg	Ala
	210				215						220				

Pro	Glu	Leu	Ile	Phe	Gly	Ala	Thr	Asp	Tyr	Thr	Ser	Ser	Ile	Asp	Val
225					230					235				240	
Trp	Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Gly	Gln	Pro	Ile	
				245					250				255		
Phe	Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val
			260					265					270		
Leu	Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr
		275					280					285			
Thr	Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Val
	290					295					300				
Phe	Arg	Pro	Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Arg	Leu
305					310					315					320
Leu	Glu	Tyr	Thr	Pro	Thr	Ala	Arg	Leu	Thr	Pro	Leu	Glu	Ala	Cys	Ala
				325					330					335	
His	Ser	Phe	Phe	Asp	Glu	Leu	Arg	Asp	Pro	Asn	Val	Lys	Leu	Pro	Asn
			340					345					350		
Gly	Arg	Asp	Thr	Pro	Ala	Leu	Phe	Asn	Phe	Thr	Thr	Gln	Glu	Leu	Ser
		355					360					365			
Ser	Asn	Pro	Pro	Leu	Ala	Thr	Ile	Leu	Ile	Pro	Pro	His	Ala	Arg	Ile
	370					375					380				
Gln	Ala	Ala	Ala	Ser	Pro	Pro	Ala	Asn	Ala	Thr	Ala	Ala	Ser	Asp	Thr
385					390					395					400
Asn	Ala	Gly	Asp	Arg	Gly	Gln	Thr	Asn	Asn	Ala	Ala	Ser	Ala	Ser	Ala
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Ser	Asn	Ser	Thr												
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<210> SEQ ID NO 3
<211> LENGTH: 2189
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct
<400> SEQUENCE: 3
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gcagcccggg cagcccgagc cccgcagcct gggcctgtgc tcggcgccat gagcggcggc
120
gggccttcgg gaggcggccc tgggggctcg ggcagggcgc ggactagctc gttcgcggag
180
ccgggcggcg gaggcggagg aggcggcggc ggccccggag gctcggcctc cggcccaggc
240
ggcaccggcg gcggaaaggc atctgtcggg gccatgggtg ggggcgtcgg ggcctcgagc
300
tccgggggtg gaccggcgg cagcggcgga ggaggcagcg gaggccccgg cgcaggcact
360
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420
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480
attggcaatg gtcatttg ggctcgtgtac caggcacggc tggcagagac cagggaacta
540
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600
cgtaagctgg accactgcaa tattgtgagg ctgagatact ttttctactc cagtggcgag
660
aagaaagacg agctttacct aaatctggtg ctggaatatg tgcccagac agtgtaccgg
720
gtggcccgcc acttcaccaa ggccaagttg accatcccta tcctctatgt caaggtgtac
780

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840 atgtaccagc ttttccgcag cttggcctac atccactccc agggcgtgtg tcaccgcgac
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 960 ggagtgcaa agcagttggt ccgaggggag cccaatgtct cctacatctg ttctcgctac
 1020 taccgggccc cagagctcat ctttgagacc actgattaca cctcatccat cgatgttttg
 1080 tcagctggct gtgtactggc agagctcctc ttgggccagc ccatcttccc tggggacagt
 1140 ggggtggacc agctggtgga gatcatcaag gtgctgggaa caccaacccg ggaacaaatc
 1200 cgagagatga accccaacta cacggagttc aagttccctc agattaaagc tcaccctg
 1260 acaaagggtg tcaaactctg aacgccgcca gaggccatcg cgctctgctc tagcctgctg
 1320 gagtacaccc catcctcaag gctctcccca cttagaggcct gtgcgcacag cttctttgat
 1380 gaactgcat gtctgggaac ccagctgcct aacaaccgcc cacttcccc tctcttcaac
 1440 ttcagtgtg gtgaactctc catccaaccg tctctcaacg ccattctcat cctcctcac
 1500 ttgaggtccc cagcgggcac taccaccctc acccgtcct cacaagcttt aactgagact
 1560 ccgaccagct cagactggca gtcgaccgat gccacaccta cctcactaa ctctctga
 1620 gggccccacc aagcaccctt ccacttccat ctgggagccc caagaggggc tgggaagggg
 1680 ggccatagcc catcaagctc ctgccctggc tggggcccta gactagaggg cagaggtaaa
 1740 tgagtccctg tccccacctc cagtccctcc ctcaccagcc tcaccctgt ggtgggcttt
 1800 ttaagaggat ttttaactgg tgtggggagg gaagagaagg acaggggtgtt ggggggatga
 1860 ggacctccta ccccttggc cccctccct ccccagacc tcacctcct ccagaccccc
 1920 tccctcctg tgtcccttgt aaatagaacc agcccagccc gtctcctctt cccttccctg
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 2040 gtccaacctg gccccgcccc tctacagct gtaactcccc tctgtcctc tgcccccaag
 2100 gtctactccc tctcacccc accctggagg gccaggggag tggagagagc tctgatgtc
 2160 ttagtttcca cagtaagggt tgctgtgta cagacctccg ttcaataaat tattggcatg
 2189 aaaacctgaa aaaaaaaaaa aaaaaaaaaa

<210> SEQ ID NO 4

<211> LENGTH: 1639

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct

<400> SEQUENCE: 4

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180   cttctgtggg agaacttaat gctgcattta tcgttaacct aacaccccaa cataaagaca
240   aaaggaaagaa aaggaggaag gaaggaaaag gtgattcgcg aagagagtga tcatgtcagg
300   gcggcccaga accacctcct ttgcggagag ctgcaagccg gtgcagcagc cttcagcttt
360   tggcagcatg aaagttagca gagacaagga cggcagcaag gtgacaacag tgggtggcaac
420   tcctgggagc ggtccagaca ggccacaaga agtcagctat acagacacta aagtgattgg
480   aaatggatca tttgggtgtg tatatcaagc caaactttgt gattcaggag aactggtcgc
540   catcaagaaa gtattgcagg acaagagatt taagaatcga gagctccaga tcatgagaaa
600   gctagatcac tgtaacatag tccgattgcg ttatttcttc tactccagtg gtgagaagaa
660   agatgaggtc tatcttaatc tgggtgctga ctatgttccg gaaacagtat acagagttgc
720   cagacactat agtcgagcca aacagacgct ccctgtgatt tatgtcaagt tgtatatgta
780   tcagctgttc cgaagtttag cctatatcca ttcctttgga atctgccatc gggatattaa
840   accgcagaac ctcttggttg atcctgatac tgctgtatta aaactctgtg actttggaag
900   tgcaaagcag ctggtccgag gagaacccaa tgtttcgtat atctgttctc ggtactatag
960   ggcaccagag ttgatctttg gagccactga ttatacctct agtatagatg tatggctctgc
1020  tggctgtgtg ttggctgagc tgttactagg acaaccaata tttccagggg atagtgggtg
1080  ggatcagttg gtagaaataa tcaaggctct gggaactcca acaagggagc aaatcagaga
1140  aatgaaccca aactacacag aatttaaatt ccctcaaatt aaggcacatc cttggactaa
1200  ggattcgtca ggaacaggac atttcacctc aggagtgcgg gtcttccgac cccgaactcc
1260  accggaggca attgcaactgt gtagccgtct gctggagtat acaccaactg cccgactaac
1320  accaaatggg cgagacacac ctgcaactct caacttcacc actcaagaac tgtcaagtaa
1380  tccacctctg gctaccatcc ttattcctcc tcatgctcgg attcaagcag ctgcttcaac
1440  cccacaaaat gccacagcag cgtcagatgc taatactgga gaccgtggac agaccaataa
1500  tgctgcttct gcatcagctt ccaactccac ctgaacagtc ccgagcagcc agctgcacag
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1620  taaaaaaaaa aaaaaaaaaa
1639

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<210> SEQ ID NO 5

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct

<400> SEQUENCE: 5